

Kazuhiko Yamasaki

List of Publications by Year in descending order

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72
papers

3,212
citations

201674

27
h-index

155660

55
g-index

74
all docs

74
docs citations

74
times ranked

4100
citing authors

#	ARTICLE	IF	CITATIONS
1	Fragment-Based Drug Discovery for <i>Trypanosoma brucei</i> Glycosylphosphatidylinositol-Specific Phospholipase C through Biochemical and WaterLOGSY-NMR Methods. <i>Journal of Biochemistry</i> , 2022, , .	1.7	1
2	Old yellow enzyme of a novel fungi-specific class. <i>FEBS Journal</i> , 2022, , .	4.7	1
3	Development of an orally-administrable tumor vasculature-targeting therapeutic using annexin A1-binding D-peptides. <i>PLoS ONE</i> , 2021, 16, e0241157.	2.5	5
4	A mixing microfluidic chip for real-time NMR monitoring of macromolecular reactions. <i>Journal of Biochemistry</i> , 2021, 170, 363-368.	1.7	1
5	Overcoming the blood-brain barrier by Annexin A1-binding peptide to target brain tumours. <i>British Journal of Cancer</i> , 2020, 123, 1633-1643.	6.4	11
6	Enhanced affinity of racemic phosphorothioate DNA with transcription factor SATB1 arising from diastereomer-specific hydrogen bonds and hydrophobic contacts. <i>Nucleic Acids Research</i> , 2020, 48, 4551-4561.	14.5	9
7	Comprehensive analysis of PPAR β agonist activities of stereo-, regio-, and enantio-isomers of hydroxyoctadecadienoic acids. <i>Bioscience Reports</i> , 2020, 40, .	2.4	16
8	Specific Coordination Mode and Electrostatic Ion Atmosphere Effects of Divalent Cations Regulating Spatially Crossing Configurations of DNA Duplexes. <i>Journal of the Physical Society of Japan</i> , 2019, 88, 044801.	1.6	0
9	Is it possible for short peptide composed of positively- and negatively-charged hydrophilic amino acid residue-clusters to form metastable hydrophobic packing?. <i>Physical Chemistry Chemical Physics</i> , 2019, 21, 9683-9693.	2.8	5
10	Structural basis for specific recognition of core fucosylation in N-glycans by <i>Pholiota squarrosa</i> lectin (PhoSL). <i>Glycobiology</i> , 2019, 29, 576-587.	2.5	8
11	Target identification reveals lanosterol synthase as a vulnerability in glioma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 7957-7962.	7.1	52
12	Crystal structures of FMN bound and FMN free forms of dihydroorotate dehydrogenase from <i>Trypanosoma brucei</i> . <i>FEBS Open Bio</i> , 2018, 8, 680-691.	2.3	7
13	NMR Biochemical Assay for Oxidosqualene Cyclase: Evaluation of Inhibitor Activities on <i>Trypanosoma cruzi</i> and Human Enzymes. <i>Journal of Medicinal Chemistry</i> , 2018, 61, 5047-5053.	6.4	5
14	The trimeric solution structure and fucose-binding mechanism of the core fucosylation-specific lectin PhoSL. <i>Scientific Reports</i> , 2018, 8, 7740.	3.3	14
15	Biochemical and structural features of extracellular vesicle-binding RNA aptamers. <i>Biomedical Reports</i> , 2017, 6, 615-626.	2.0	8
16	Simulated Annealing-Extended Sampling for Multicomponent Decomposition of Spectral Data of DNA Complexed with Peptide. <i>Journal of the Physical Society of Japan</i> , 2017, 86, 014802.	1.6	0
17	Development of new fusion proteins for visualizing amyloid- β oligomers in vivo. <i>Scientific Reports</i> , 2016, 6, 22712.	3.3	32
18	The combination of sequence-specific and nonspecific DNA-binding modes of transcription factor SATB1. <i>Biochemical Journal</i> , 2016, 473, 3321-3339.	3.7	9

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19	An NMR Biochemical Assay for Fragment-Based Drug Discovery: Evaluation of an Inhibitor Activity on Spermidine Synthase of <i>Trypanosoma cruzi</i> . <i>Journal of Medicinal Chemistry</i> , 2016, 59, 2261-2266.	6.4	8
20	Structures, Functions, and Evolutionary Histories of DNA-Binding Domains of Plant-Specific Transcription Factors. , 2016, , 57-72.		1
21	Analysis of ATP and AMP binding to a DNA aptamer and its imidazole-tethered derivatives by surface plasmon resonance. <i>Analyst</i> , The, 2015, 140, 5881-5884.	3.5	9
22	Tracing Primordial Protein Evolution through Structurally Guided Stepwise Segment Elongation. <i>Journal of Biological Chemistry</i> , 2014, 289, 3394-3404.	3.4	14
23	Real-Time NMR Monitoring of Protein-Folding Kinetics by a Recycle Flow System for Temperature Jump. <i>Analytical Chemistry</i> , 2013, 85, 9439-9443.	6.5	9
24	DNA-binding domains of plant-specific transcription factors: structure, function, and evolution. <i>Trends in Plant Science</i> , 2013, 18, 267-276.	8.8	229
25	Domain Structures and Inter-Domain Interactions Defining the Holoenzyme Architecture of Archaeal D-Family DNA Polymerase. <i>Life</i> , 2013, 3, 375-385.	2.4	4
26	Structural Basis for Sequence-specific DNA Recognition by an Arabidopsis WRKY Transcription Factor. <i>Journal of Biological Chemistry</i> , 2012, 287, 7683-7691.	3.4	95
27	Solution structure of the N-terminal domain of the archaeal D-family DNA polymerase small subunit reveals evolutionary relationship to eukaryotic B-family polymerases. <i>FEBS Letters</i> , 2010, 584, 3370-3375.	2.8	14
28	Effect of Glycosylation on <i>Cis</i> / <i>Trans</i> Isomerization of Prolines in IgA1-Hinge Peptide. <i>Journal of the American Chemical Society</i> , 2010, 132, 5548-5549.	13.7	25
29	Glycerol stimulates innate chaperoning, proteasomal and stress-resistance functions: implications for geronto-manipulation. <i>Biogerontology</i> , 2008, 9, 269-282.	3.9	14
30	Structures and evolutionary origins of plant-specific transcription factor DNA-binding domains. <i>Plant Physiology and Biochemistry</i> , 2008, 46, 394-401.	5.8	80
31	Structural basis for recognition of the matrix attachment region of DNA by transcription factor SATB1. <i>Nucleic Acids Research</i> , 2007, 35, 5073-5084.	14.5	44
32	Stress Chaperones, Mortalin, and Pex19p Mediate 5-Aza-2' Deoxycytidine-Induced Senescence of Cancer Cells by DNA Methylation-Independent Pathway. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2007, 62, 246-255.	3.6	29
33	Mortalin sensitizes human cancer cells to MKT-077-induced senescence. <i>Cancer Letters</i> , 2007, 252, 259-269.	7.2	79
34	Cell-free synthesis of zinc-binding proteins. <i>Journal of Structural and Functional Genomics</i> , 2007, 7, 93-100.	1.2	34
35	An Arabidopsis SBP-domain fragment with a disrupted C-terminal zinc-binding site retains its tertiary structure. <i>FEBS Letters</i> , 2006, 580, 2109-2116.	2.8	45
36	Structural and Functional Differences between Mouse Mot-1 and Mot-2 Proteins That Differ in Two Amino Acids. <i>Annals of the New York Academy of Sciences</i> , 2006, 1067, 220-223.	3.8	11

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37	Geroprotection by Glycerol: Insights to Its Mechanisms and Clinical Potentials. <i>Annals of the New York Academy of Sciences</i> , 2006, 1067, 488-492.	3.8	13
38	Solution Structure and DNA-binding Mode of the Matrix Attachment Region-binding Domain of the Transcription Factor SATB1 That Regulates the T-cell Maturation. <i>Journal of Biological Chemistry</i> , 2006, 281, 5319-5327.	3.4	24
39	Solution Structure of an Arabidopsis WRKY DNA Binding Domain. <i>Plant Cell</i> , 2005, 17, 944-956.	6.6	185
40	Solution Structure of the Major DNA-binding Domain of Arabidopsis thaliana Ethylene-insensitive3-like3. <i>Journal of Molecular Biology</i> , 2005, 348, 253-264.	4.2	82
41	Solution Structure of the B3 DNA Binding Domain of the Arabidopsis Cold-Responsive Transcription Factor RAV1 [W]. <i>Plant Cell</i> , 2004, 16, 3448-3459.	6.6	107
42	10 Residue Folded Peptide Designed by Segment Statistics. <i>Structure</i> , 2004, 12, 1507-1518.	3.3	278
43	Structural and sequence comparisons arising from the solution structure of the transcription elongation factor NusG from <i>Thermus thermophilus</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 56, 40-51.	2.6	30
44	Nature of the Chemical Bond Formed with the Structural Metal Ion at the A9/G10.1 Motif Derived from Hammerhead Ribozymes. <i>Journal of the American Chemical Society</i> , 2004, 126, 744-752.	13.7	28
45	A Novel Zinc-binding Motif Revealed by Solution Structures of DNA-binding Domains of Arabidopsis SBP-family Transcription Factors. <i>Journal of Molecular Biology</i> , 2004, 337, 49-63.	4.2	267
46	Acid-induced denaturation of <i>Escherichia coli</i> ribonuclease HI analyzed by CD and NMR spectroscopies. <i>Biopolymers</i> , 2003, 69, 176-188.	2.4	6
47	A modified sensor chip for surface plasmon resonance enables a rapid determination of sequence specificity of DNA-binding proteins. <i>FEBS Letters</i> , 2003, 536, 151-156.	2.8	19
48	Molecular Structure and Novel DNA Binding Sites Located in Loops of Flap Endonuclease-1 from <i>Pyrococcus horikoshii</i> . <i>Journal of Biological Chemistry</i> , 2002, 277, 37840-37847.	3.4	29
49	Identification of the Metal Ion Binding Site on an RNA Motif from Hammerhead Ribozymes Using 15N NMR Spectroscopy. <i>Journal of the American Chemical Society</i> , 2002, 124, 4595-4601.	13.7	52
50	Determinants in the Sequence Specific Binding of Two Plant Transcription Factors, CBF1 and NtERF2, to the DRE and GCC Motifs. <i>Biochemistry</i> , 2002, 41, 4202-4208.	2.5	98
51	NMR Structure of Ribonuclease HI from <i>Escherichia coli</i> . <i>Biological and Pharmaceutical Bulletin</i> , 2000, 23, 1147-1152.	1.4	11
52	A novel mode of DNA recognition by a β -sheet revealed by the solution structure of the GCC-box binding domain in complex with DNA. <i>EMBO Journal</i> , 1998, 17, 5484-5496.	7.8	426
53	Structural stability and internal motions of <i>Escherichia coli</i> ribonuclease HI: 15 N relaxation and hydrogen-deuterium exchange analyses 1 Edited by P. E. Wright. <i>Journal of Molecular Biology</i> , 1998, 277, 707-722.	4.2	14
54	Pressure-Denatured State of <i>Escherichia coli</i> Ribonuclease HI As Monitored by Fourier Transform Infrared and NMR Spectroscopy. <i>Biochemistry</i> , 1998, 37, 18001-18009.	2.5	16

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55	Zinc finger proteins of the archaebacterial origin. Proceedings of the Japan Academy Series B: Physical and Biological Sciences, 1998, 74, 227-232.	3.8	0
56	Methylation of adenine bases at the N ⁶ H ₂ groups decreases the melting temperature of the DNA duplex independently of the nucleotide sequence. Proceedings of the Japan Academy Series B: Physical and Biological Sciences, 1998, 74, 210-215.	3.8	3
57	Regional Polyesterism in the GTP-Bound Form of the Human c-Ha-Ras Protein., Biochemistry, 1997, 36, 9109-9119.	2.5	168
58	Solution structure of an extracellular domain containing the WSxWS motif of the granulocyte colony-stimulating factor receptor and its interaction with ligand. Nature Structural Biology, 1997, 4, 498-504.	9.7	33
59	DNA recognition by β -sheets. Biopolymers, 1997, 44, 335-359.	2.4	29
60	DNA recognition by β -sheets. Biopolymers, 1997, 44, 335-359.	2.4	1
61	Application of the quasi-spectral density function of ¹⁵ N nuclei to the selection of a motional model for model-free analysis. Journal of Biomolecular NMR, 1995, 6, 423-6.	2.8	7
62	Spectral densities of nitrogen nuclei in Escherichia coli ribonuclease HI obtained by ¹⁵ N NMR relaxation and molecular dynamics. Journal of Biomolecular NMR, 1995, 6, 217-220.	2.8	18
63	Ligand Binding Characteristics of the Carboxyl-terminal Domain of the Cytokine Receptor Homologous Region of the Granulocyte Colony-stimulating Factor Receptor. Journal of Biological Chemistry, 1995, 270, 27845-27851.	3.4	21
64	Characterization of the internal motions of Escherichia coli ribonuclease HI by a combination of ¹⁵ N-NMR relaxation analysis and molecular dynamics simulation: examination of dynamic models. Biochemistry, 1995, 34, 6587-6601.	2.5	61
65	Folding Pathway of Escherichia coli Ribonuclease HI: A Circular Dichroism, Fluorescence, and NMR Study. Biochemistry, 1995, 34, 16552-16562.	2.5	69
66	Site-directed mutagenesis, fluorescence, and two-dimensional NMR studies on microenvironments of effector region aromatic residues of human c-Ha-Ras protein. Biochemistry, 1994, 33, 65-73.	2.5	36
67	Mutations that abolish the ability of Ha-Ras to associate with Raf-1. Oncogene, 1994, 9, 2153-7.	5.9	56
68	Sequence-specific ¹ H and ¹⁵ N resonance assignments and secondary structure of GDP-bound human c-Ha-Ras protein in solution. Journal of Biomolecular NMR, 1993, 3, 165-84.	2.8	24
69	Guanine-nucleotide binding activity, interaction with GTPase-activating protein and solution conformation of the human c-Ha-Ras protein catalytic domain are retained upon deletion of C-terminal 18 amino acid residues. The Protein Journal, 1992, 11, 731-739.	1.1	8
70	¹ H- ¹⁵ N NMR study of human c-Ha-ras protein: Biosynthetic incorporation of ¹⁵ N-labeled amino acids. Journal of Biomolecular NMR, 1992, 2, 71-82.	2.8	18
71	Spin-labeling proton NMR study on aromatic amino acid residues in the guanine nucleotide binding site of human c-Ha-ras(1-171) protein. Biochemistry, 1989, 28, 9550-9556.	2.5	12
72	Conformation change of effector-region residues in antiparallel β -sheet of human c-Ha-ras protein on GDP \rightarrow GTP \rightarrow GTP \rightarrow S exchange: A two-dimensional NMR study. Biochemical and Biophysical Research Communications, 1989, 162, 1054-1062.	2.1	35